## CLAIM AMENDMENTS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Claims 1-13 (cancelled)

14. (previously presented) A method comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise a plurality of different target analytes from a first individual and the microspheres of said second subpopulation comprise a plurality of different target analytes from a second individual, and wherein a plurality of said different target analytes are covalently attached to each of said microspheres,

wherein said microspheres are distributed on said surface;

b) contacting said array composition with a first set of readout probes; and

c) detecting the presence of a first target analyte.

15. (original) The method according to claim 14 further comprising:

d) contacting said array composition with a second set of readout probes;

e) detecting the presence of a second target analyte.

16. (original) The method according to claim 14, wherein said microspheres are randomly distributed on said surface.

17. (original) The method according to claim 14, wherein said first set of readout probes comprises at least first and second readout probes, wherein said first and second readout probes comprise first and second labels, respectively.

18. (original) The method according to claim 17, further comprising detecting said first label as an indication of the presence of said first target analyte.

19. (cancelled)

20. (cancelled)

21. (currently amended) A method of genotyping comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise at least first and second different target nucleic acid molecules ~~sequences~~ from a first individual and the microspheres of said second subpopulation comprise at least first and second different target nucleic acid molecules ~~sequences~~ from a second individual, wherein said at least first and second different target nucleic acid molecules ~~sequences~~ are covalently attached to each of said microspheres with first and second attachment moieties, respectively;

wherein said microspheres are randomly distributed on said surface;

b) contacting said array composition with a first set of extension probes that hybridize with at least said first target nucleic acid molecules ~~sequence~~ adjacent to a first detection position to form an extension complex;

c) contacting said extension complex with a composition comprising

i) at least a first nucleotide;

ii) polymerase;

wherein said polymerase extends a first extension probe with said first nucleotide when said first nucleotide is complementary to said first detection position ~~of said first target sequence~~; and

d) detecting the presence of said first nucleotide, whereby said genotype is determined.

22. (original) The method according to claim 21, wherein said first nucleotide comprises a label.

23. (currently amended) A method of determining the identification of a nucleotide at a detection position in at least a first target nucleic acid molecule ~~sequence~~ comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise a plurality of different target nucleic acid molecules ~~sequences~~ from a first individual and the microspheres of said second subpopulation comprise a plurality of different target nucleic acid molecules ~~sequences~~ from a second individual, and wherein a plurality of said different target nucleic acid molecules [sequences] are covalently attached to each of said microspheres, wherein said microspheres are distributed on said surface;

b) forming a first hybridization complex between said first target nucleic acid molecule ~~sequence~~ and at least a first readout probe; and

c) determining the nucleotide at said detection position.

24. (currently amended) The method according to claim 23, wherein said first target nucleic acid molecule ~~sequence~~ comprises a first and a second target domain, wherein said first hybridization complex comprises said first target nucleic acid molecule ~~sequence~~, a first readout probe hybridized to said first domain and a second readout probe hybridized to said second domain, wherein at least one of said readout probes comprise a label said determining comprises adding a ligase to form a ligation complex.

25. (original) The method according to claim 24, wherein said first readout probe comprises a detectable label.

26. (currently amended) The method according to claim 23, further comprising contacting said hybridization complex with at least a first nucleotide and a polymerase, wherein said polymerase extends said first readout probe with said first nucleotide when said first nucleotide is complementary to said first detection position ~~of said first target sequence~~.

27. (previously presented) The method according to claim 14, 21 or 23 wherein said substrate is a fiber optic bundle.

28. (previously presented) The method according to claim 14, 21 or 23 wherein said substrate is selected from the group consisting of glass and plastic.

29. (previously presented) The method according to claim 14, 21, or 23 further comprising contacting said microspheres with decoder binding ligands, wherein the microspheres of each subpopulation comprises an identifier binding ligand that will bind a decoder binding ligand for identification and elucidation of said target analyte.

30. (previously presented) The method according to claim 14, wherein said target analytes comprise target sequences.

31. (currently amended) The method according to claim 30, wherein said target analytes ~~sequences~~ comprise target nucleic acids.

32. (previously presented) The method according to claim 31, wherein said target nucleic acids comprise target genomic DNA.

33. (cancelled)

34. (currently amended) The method according to claim 21 or 23 ~~33~~, wherein said target nucleic acids comprise target genomic DNA.

35. (currently amended) A method comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of ~~of~~ said first subpopulation comprise a plurality of different target analytes from a first individual and the microspheres of said second subpopulation comprise a plurality of different target analytes from a second individual, wherein a plurality of different target analytes are attached to each of said microspheres via receptor-ligand interaction, wherein said target analytes are derivatized with said receptor or said ligand, and wherein said microspheres are distributed on said surface;

b) contacting said array composition with a first set of readout probes; and

c) detecting the presence of a first target analyte.

36. (currently amended) A method of genotyping comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise at least first and second different target nucleic acid molecules ~~sequences~~ from a first individual and the microspheres of said second subpopulation comprise at least first and second different target nucleic acid molecules ~~sequences~~ from a second individual, wherein said plurality of first and second different target nucleic acid molecules ~~sequences~~ are attached to each of said microspheres via receptor-ligand interaction; wherein said target analytes are derivatized with said receptor or said ligand,

wherein said microspheres are randomly distributed on said surface;

b) contacting said array composition with a first set of extension probes that hybridize with at least said first target nucleic acid molecule ~~sequence~~ adjacent to a first detection position to form an extension complex;

c) contacting said extension complex with a composition comprising

i) at least a first nucleotide;

ii) polymerase;

wherein said polymerase extends a first extension probe with said first nucleotide when said first nucleotide is complementary to said first detection position ~~of said first target sequence~~; and

d) detecting the presence of said first nucleotide, whereby said genotype is determined.

37. (currently amended) A method of determining the identification of a nucleotide at a detection position in at least a first target nucleic acid molecule ~~sequence~~ comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise a plurality of different target nucleic acid molecules ~~sequences~~ from a first individual and the microspheres of said second subpopulation comprise a plurality of different target nucleic acid molecules ~~sequences~~ from a second individual, wherein said plurality of different

target nucleic acid molecules ~~sequences~~ are attached to each of said microspheres via receptor-ligand interaction, wherein said target nucleic acid molecules ~~analytes~~ are derivatized with said receptor or said ligand,

wherein said microspheres are distributed on said surface;

b) forming a first hybridization complex between said first target nucleic acid molecule ~~sequence~~ and at least a first readout probe; and

c) determining the nucleotide at said detection position.

38. (previously presented) The method according to claim 35, 36 or 37, wherein said receptor is streptavidin and said ligand is biotin.

39. (previously presented) The method according to claim 38, wherein said microspheres are streptavidin coated.